

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 27, 2001, 17:07:35 ; Search time 2462.53 Seconds
(without alignments)
2690.912 Million cell updates/sec

Title: US-09-784-340-3_COPY_7800_8500

Perfect score: 701
Sequence: 1 ggtgtggtcgaatgagagaaaa.....taggattccagaaaaaatra 701

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST: *
1: gb_est1:*
2: gb_est2:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Db 8 ACAA 5

RESULT	2
LOCUS	A0319346/c
DEFINITION	A0319346 667 bp DNA Homo sapiens genomic clone RPCI-11-99P4, DN RPCI11-99P4.TV RPCI-11 Homo sapiens genomic clone RPCI-11-99P4, DN
ACCESSION	A0319346
VERSION	A0319346
KEYWORDS	GSS.
SOURCE	human.
ORGANISM	Homo sapiens

BASE COUNT	152 a	181 c	118 g	216 t
ORIGIN				

Query Match	19.9%	Score 139.4;	DB 227;	Length 667;	
Best Local Similarity	59.9%	Pred: No. 1.1e-25;			
Matches 348;	Conservative	0;	Mismatches 211;	Indels 22;	Gaps 6

[illegible]

Db	343	TAGATTTCCTCCAGGAGGATTCTAATTTGTAAAGTTAAAGCAACAGGCACAAAGTTCCATG	284
Qy	290	gaagcattctgaagactgaaagat-----agtcacttctgctatctgaacgaattctg	342
Db	283	GATCCATACGCTGTGCTAAAGAGGTCACGCGGTATCTGTG-46TTCATTGTAGGCAATGGG	224
Qy	343	atcagttattcaagcccaagtagctglatcattgttc--cataaggtggtctaccag	400
.Db	223	GTCAGTGGGGCAAG-TCAAGTAGGTTGTACTTCTGCTTCCACACAGAGGTGTACACAGA	165
Qy	401	aggcagttgtgaagtaaaatcctgactgaaacacattgaagaaatggaagaggttggaag	460
Db	164	TGATGTTGCTGTAAAGTAAATATATCTAATATAGCCACATAG-36GAAACAGACACAGAAAGA	105
Qy	461	attttaacggtgtgcagtgttgaactgaagactggtttgtg-atg-gaaaatcaactat	519
Db	104	ACTGGAACCTGTGTCAAAGGTGACTAAAGCCCTCTTCGg-ATGAGAAAGTCCATTTCAT	45
Qy	520	attttaaatgcatagccagacacataaaattatgaagat-560	
Db	44	ATTCAATATGATGTTGAGGCAATATATAAATTAATGAGATTC-4	

RESULT	3
LOCUS	B46805
DEFINITION	BA6805 397 bp DNA GSS 21-OCT-1997
ACCESSION	HS-1066-A1-C09-MR.ab1 CIT Human Genomix: GSS Library C Homo
VERSION	sapiens genomic clone Plate=CT 270 Col=17 Row=E, DNA sequence.
KEYWORDS	B46805
SOURCE	BA6805.1 GI:2551639
ORGANISM	GSS.
REFERENCE	human.
AUTHORS	Homo sapiens
TITLE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 397)
JOURNAL COMMENT	Mahairas,G.G., Zackrone,K.D., Smith,T., Tipton,S., Schmidt,S., Traicoff,R., Abajian,C., Blanchard,A., West,A. and Hood,L.E. Construction of a Characterized Clone Resource for Genomic Sequencing: Generation and Preliminary Analysis of 20,000 Sequence Tagged Connectors Unpublished (1997)
	Contact: Mahairas GG, Zackrone KD, Hood L University of Washington Seattle, WA 98195, USA
	Tel: (206) 616-8744
	Fax: (206) 685-7301
	Email: kzackrone@u.washington.edu
	Sequence Tagged Connector
	Plate: CT 270 row: E column: 17
	Class: BAC ends
	High quality sequence stop: 397.

FEATURES	source	Location/Qualifiers
		1. .397
		/organism="Homo sapiens"
		/db_xref="taxon:9606"
		/clone="plate=Ct 270 Col-17 Row=E"
		/clone_1fb="Ct Human Genomic Sperm Library C"
		/sex="M"
		/note="Organ: sperm; Vector: pBeloBAC11; BAC clones in E-coli DH10B"
BASE COUNT		113 a 65 c 108 g 111 t
ORIGIN		

Query Match	19.88%	Score 138.6;	DB 256;	Length 397;
Best Local Similarity	67.48%	Pred. No. 1.5e-25;		
Matches 242;	Conservative	0;	Mismatches 109;	Indels 8;
				Gaps 3

OY 217 ggtgaacctagtggtglttccaatgggaaactgtaatgttagtgtttaaycaagcagg 276
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 26 GGTATCATCTAGTGGGTCCTCCCAATTGGGAATTGTAACGTGGTAGAATTACAGCACAAGCTGG 85

OY	277	cacaagtcacatgaggcgcttcgcgaacgcyaagaatgatcacttggcatatctgca--c	334	
Db	86	ATCAAACTTCACATCCAGTATCACACTGTGACTATAAAGTGCGTTGGCTTATCTGCATTGG	145	
OY	335	agaattcgtatcagtgtattcaagcccaagttaagtgctatctagtcttctaagtggtt	394	
Db	146	TGCATGTAGAGAGGTGGAGGTCACATTAGTATGATCATCTAGCTGCTCATTAGGCCAATG	205	
OY	395	accaggaagcgatgttgttaagtaa-----aaatctcgtacgaacacatltggaaatgaa	449	
Db	206	GTCACATGAAGAAGTGTTATTAATGAAGGAGACATCTGATTCACACTTTGAGGAACCTGG	265	
OY	450	ggaagtggaagaattttaaacggttcgaatggtttaccaagaacctgcttcgtattg-9aaa	508	
Db	266	GGAGGACAGAACAACTGGAATTTGTTGTATAGAGATACCTAAGCCTCTGCTACTATTTGACAAA	325	
OY	509	attcaactataatttaaatgcatagccacacacataaaatatlaagaatttaccca	567	
Db	326	GTTAATCTCATATTTTTCACATGATGATGCTGAGGCAACATTAACCTGTAAATTCACACA	384	
RESULT	4	AQ264450	678 bp DNA GSS	27-OCT-1998
LOCUS		CITBI-EI-2509C10.TF CITBI-EI Homo sapiens genomic clone 2509C10,		
DEFINITION		DNA sequence.		
ACCESSION		AQ264450		
VERSION		AQ264450.1 GI:3792817		
KEYWORDS		GSS.		
SOURCE		human.		
ORGANISM		Homo sapiens		
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
		1 (bases 1 to 678)		
		Adams,M.D., Kounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,		
		Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and		
		Venter,J.C.		
TITLE		Use of a random human BAC End Sequence database for Sequence-Ready		
JOURNAL		Map Building		
COMMENT		Unpublished (1998)		
		Other_GSSs: CITBI-EI-2509C10.TF		
		Contact: Mark Adams		
		Department of Eukaryotic Genomics		
		The Institute for Genomic Research		
		9712 Medical Center Dr., Rockville, MD 20850, USA		
		Tel: 301 838 0200		
		Fax: 301 838 0208		
		Email: mdadams@ligr.org		
		Clones are available from Research Genetics (info@resgen.com), BAC		
		End search page:		
		http://www.ligr.org/lcd/humgen/bac_end_search/bac_end_search.html.		
		Seq primer: M3-21		
		Class: BAC ends.		
FEATURES		Location/Qualifiers		
SOURCE		1..678		
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		/clone_1lb="CITBI-EI"		
		/sex="male"		
		/cell_type="sperm"		
		/note="Vector: pBelOAC11; Site_1: EcoRI; Site_2: EcoRI;		
		Caltech Human BAC Library D"		
BASE COUNT		163 a 184 c 117 g 214 t		
ORIGIN				
Query Match		19.6%; Score 137.4; DB 226; Length 678;		
Best Local Similarity		60.0%; Pred. No. 3.5e-25;		
Matches		326; Conservative 0; Mismatches 196; Indels 21; Gaps		
OY	1	gtgtgtgtcgaatggaacacatggtggaacactcaacacacataaataacagaaac	60	

[illegible]

[illegible]

OY	304		ctgaagaatagtcacatttgggatctcgcacgaactcgu..cagtgaattcaagc-----	357
Db	266	CTGACAGGAGGTCACTATGCATFATTCACGACGTCCATGTGGGGTACAAAGGCTTGACGA	207	
OY	358		-----ccaagttagctcatctagtgttgccctaaggatggtttaccaggaggcagtglt-	411
Db	206	GTGATCTCACATRAGCGTTGTTCTAGCTGTGTCCTATTAGAAGC...TGICATCAAAAAAGCAGTTG	147	
OY	412		---aaagtaaaaatcctcyactgaacacatlgaggaatatgtaggaagtgaagatttaa	467
Db	146	TGAAGGCGAGATATCTGGATCATCATCACAAGTAAGTGGTAGAGATTGAGATTGAG	87	
OY	468		acggtgtcagtggttacctcaaacgccgtcttcgtgtg- gaanaatcaactataatttaa	526
Db	86	ACTATATATA---AAGGTAATTCTCGTTTCTGATGTGAGAAAGTCCAAATTTAAATTTAAA	31	
OY	527		atgcatagcacagcacacataaatattaag 556	
Db	30	ATAAAGCTTAGGCCAACATGGGATTATTAG 1		
RESULT	8			
LOCUS	AO506793/C	624 bp DNA	GSS	29-APR-1999
DEFINITION	RPC1-11-293D20.TV RPC1-11 Homo sapiens genomic clone RPC1-11-293D20			
ACCESSION	AJ0506793			
VERSION	AJ0506793			
KEYWORDS	AJ0506793.1 GI:4711540			
SOURCE	GSS.			
ORGANISM	human.			
	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
REFERENCE	1 (bases 1 to 624)			
AUTHORS	Zhao,S., Adams,M.D., Niernan,W., Malek,J., de Jong,P. and Venter,J.C.			
TITLE	Use of BAC End Sequences from Library RPC1-11 for Sequence-Ready Map Building			
JOURNAL	Unpublished (1997)			
COMMENT	Contact: Shaying Zhao, William Niernan, Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MA. 20850 Tel: 301 838 0200 Fax: 301 838 0208 Email: hbe@ligr.org Clones are derived from the human BAC library RPC1-11. For BAC library availability, please contact Peter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.com , bio.falo.edu/ordering) or from Research Genetics (http://www.rgen.com). P.-J. end search page: http://www.tlgr.org/tldb/humgen/bac_end_search/bac_end_search.html . Seq primer: T7 Class: BAC ends.			
FEATURES				
source				
	Location/Qualifiers			
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	/db_xref="taxon:9606"			
	/clone="RPC1-11-293D20"			
	/clone_id="RPC1-11"			
	/sex="Male"			
	/cell_type="Lymphocytes"			
	/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI; RPC11 Human Male BAC Library"			
BASE COUNT	127 a 178 c 124 g 195 t			
ORIGIN				
Query Match	17.9%	Score 125.4	DB 229	Length 624
Best Local Similarity	56.6%	Pred. NO. 4.4e-22		
Matches 303; Conservative	0	Mismatches 191;	Indels 23	Gaps 4

OY	16	gaataacttgaggaaacttaaccacacataaaacaagaacatcttccttggacca	75
Db	520	GAGAAAGAGAAGCAACTCACAAAATTCATGTAACATCAGAAAGC---TTTCTTAAG	464
OY	76	tlttcitagagaaaagtccagcalccctcgtttaaggccacttagaagaanaaatctctg	135
Db	463	ATCCAGAGAGAGAAGGAAGGCAGCATGGCTTCACAGAGGCCATGGGAAAGAGAGCCACAG	404
OY	136	ggaaagacattccaacctgaatgatgaagcaaacgaagaagatgtaggcattatgctc	195
Db	403	GGAAMACAAGGTTCAAAACACTGGATGGGGAACAAGAGAGAACAAGGAGACCTACGGGCTC	344
OY	196	aaaaigttaacttggactccagggtgttaacctagttgtgttccaattggnaactlaatt	255
Db	343	AAAGTGTTCAATTGGAGAGTCCAGCAAGCATTTATCCACAGCAGGCTTCCCAAGSGGAGTTTAA	284
OY	256	gtatagtttaataagcaagcaagcaaaagtcocatgatgaagcatctcagactgaagaatg	315
Db	283	-----GATTAGAGCGCAGCAGCATAGCTCCGTCAGTATCTCTGCAACTGAGACATAT	229
OY	316	cacttggcatactatcgacagaatctgcatalcagtatcca-----agcccaga	364
Db	228	CACGTGGCACATCTGTGAGATCCATGCTGGGGGTGGGAGTCAGTCAAGCTAAGTCAAGTA	169
OY	365	gacctatcattgtgttcctataggtgtgttaccaagaggaagtgatlaa----gtaaaa	420
Db	168	GGTTGTATCCAGCTGTCTCATAGAAAGTGTGTAGCAGAGGAGATGATTATAGGCGCAGATG	109
OY	421	tctctactgaacacattgaggaaaatggaagagtggaagatttaaacygtctaagt	480
Db	108	TCCAGGTCAACCATGCTCAGGAATGGGAGACAGTAAACACTPAGGACCACATGACAAAGG	49
OY	481	tgaactaagactgcttgtgtatgagaanaattcaact	517
Db	48	TGACAAGAGAGTGAACCTTATTTCAAGTAGATTT	12
RESULT	9		
LOCUS	A0322289/c		
DEFINITION	RFC111-109L5.TV RFC1-11 Homo sapiens genomic clone RFC1-11-109L5, DNA sequence.	GSS	06-MAY-1999
ACCESSION	A0322289		
VERSION	A0322289.1	GI:4054869	
KEYWORDS	GSS.		
SOURCE	human.		
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. 1 (bases 1 to 759) Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Sub,E., Wible,C., de Jong,P. and Venter,J.C Use of human BAC End Sequences for Sequence-Ready Map Building Unpublished (1998) Contact: Shaying Zhao, William Nierman, Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850 Tel.: 301 838 0200 Fax: 301 838 0208 Email: jhe@tigr.org Clones are derived from the human BAC library RFC1-11. For BAC library availability, please contact Pieter de Jong (pietere@jeng.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering/) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html Seq primer: T7 Class: BAC ends.		
TITLE			
JOURNAL			
COMMENT			
FEATURES			
Source	Location/Qualifiers		
	1..759	/organism="Homo sapiens"	

[illegible]

OY 553 taagaatt 560
 Db 15 CAGGAAGT 8

RESULT 12
 LOCUS A0090754/c 406 bp DNA GSS 26-AUG-1998
 DEFINITION HS_3008_B1_H02.T7 CIT Approved Human Genomic Sperm Library D Homo
 sapiens genomic clone Plate=3008 Col=3 Row=P, DNA sequence.
 ACCESSION A0090754
 VERSION A0090754.1 GI:3459665
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
 Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
 Hood,L.

TITLE
 JOURNAL Sequence-tagged connectors: A sequence approach to mapping and
 MEDLINE scanning the human genome
 COMMENT Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)

CONTACT: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Sequence Tagged Connector
 Plate: 3008 row: P column: 3
 Class: BAC ends
 High quality sequence stop: 406.
 Location/Qualifiers

FEATURES
 source 1..406
 /organism="Homo sapiens"
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 /clone_lib="CIT Approved Human Genomic Sperm Library D"
 /sex="male"
 /note="Organ: sperm; Vector: pBelobAC11; BAC Clones in
 E-Coli DH10B"

BASE COUNT 83 a 129 c 84 g 110 t
 ORIGIN

Query Match 15.0%; Score 105.2; DB 224; Length 406;
 Best Local Similarity 58.2%; Pred. No. 6.8e-17;
 Matches 226; Conservative 0; Mismatches 153; Indels 9; Gaps 2;

OY 77 ttctagaagaagaagtcagcattcgttaagccactaggaagaagaattctctg 136
 Db 397 TCCACAGACACACAGGACATGACTCACAGGCGCAATGGAACATATCCAG 338
 OY 137 gaaagaacattcaacaaatgaatgaagacaaagaagatgagatctatgtgcca 196
 Db 337 GACATCCATGACAGATGACCAATGGGAGACAGACACAGACACACACACAC 282
 OY 197 aaatgttaactgagatcagaagtgcttaactaggttggtttcccaatgaggaactgttaattg 256
 Db 281 AAGCTTACTGAGGTCCAGGCGCTTCCAGTAGTTCATGACGAGTCTTAAGTG 222
 OY 257 gtatgttaatgaagcagacacaagaatgcattgagagcattctgagactggaagaatagtc 316
 Db 221 GTGGGTTTACAGCAAGACAGATATGAGCTGTGTGGGCTTGTCCGCTGCTAGAGGTGCTC 162
 OY 317 acttggcatatctgcacagaatctgtatcagtgatccaagcccaagagctgatatcag 376
 Db 161 ACTGCACAGTTCATGATGGGCTGTGGGCTCAGTGGGCTGAGTCAAGCAGGTTGTATCTAG 102

OY 377 ttgtccatagagtggttaccagagagcagtg-----tg 39taaaaaactcctactgaa 431
 Db 101 CTGACCCATGGGAGGAGGCGTCCACGAGAGTGTCATTTTTCGCAATATCTGCAATAC 42
 OY 432 cacattgagaatcgaagagagtgga 459
 Db 41 CACTTTGAGAGTGTGAGACAGAGAA 14

RESULT 13
 LOCUS A0155005/c 467 bp DNA GSS 16-OCT-1998
 DEFINITION HS_3039_B1_A04.MF CIT Approved Human Genomic Sperm Library D Homo
 sapiens genomic clone Plate=3039 Col=7 Row=B, DNA sequence.
 ACCESSION A0155005
 VERSION A0155005.1 GI:3547675
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
 Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
 Hood,L.

TITLE
 JOURNAL Sequence-tagged connectors: A sequence approach to mapping and
 MEDLINE scanning the human genome
 COMMENT Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)

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 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Sequence Tagged Connector
 Plate: 3039 row: B column: 7
 Class: BAC ends
 High quality sequence stop: 467.
 Location/Qualifiers

FEATURES
 source 1..467
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="Plate=3039 Col=7 Row=B"
 /clone_lib="CIT Approved Human Genomic Sperm Library D"
 /sex="male"
 /note="Organ: sperm; Vector: pBelobAC11; BAC Clones in
 E-Coli DH10B"

BASE COUNT 109 a 128 c 78 g 147 t 5 others
 ORIGIN

Query Match 14.7%; Score 103.2; DB 224; Length 467;
 Best Local Similarity 58.7%; Pred. No. 2.3e-16;
 Matches 256; Conservative 0; Mismatches 165; Indels 15; Gaps 4;

OY 143 cacattcaaccaatgaatgaagacaaagaagaagatgagagatctatgtgccaatgt 202
 Db 466 CATACACACAGGCGGAGGAGCAAAAGAGAGACATATGACTGTGCTTGAGGCAT 407
 OY 203 taactggatccagagtgcttaccataggttggtttcccaatgaggaactgttaattgtgtgt 262
 Db 406 TTATTGGGACNCAGGCTTTTACGCAAGAAAGTTTCCACACAGACTTCTAAGTGTAGGT 347
 OY 263 ttaatgcaagcagacaaagatccatgagagcattctgagactgaagaatagtgca----- 317
 Db 346 TTAGAGCAATCATGATAGTATGATCCATGAGGACAGGTTATCTTACAGAGCTGCTACAGCA 287
 OY 318 ----cttggcatatctgcacagaatctgatatcagtgatccaagcccaagtaagctgtatct 374
 Db 286 TATCTGTATGATCATATGCGCTGTAGGCGTTCAGTGGTACAGTGGTACAGCAAGCAATGTATCT 227

us-09-784-3_copy_7800_8500.rst

QY	270	aagcagcacaacgaatccatcttgtaggagcattcgaagatgc...	atagtcacttggcatc 329
Db	291	AAGCAGGAGATGATGTTCCAGAGAGTGCGCACAGTGAATGAM...	ATGGGCCCTGTGGCGCATC 232
QY	330	tgcaaa--gaatcgtatcagatcgaattcaagcccaagtagc...	ttactagttgcctctag 387
Db	231	TGCACATTCCTAGGTGGGGGTGTGAGGGGTGATGCTGGCCAA...	AGTTCTTAGCTGTGCAATAG 172
QY	388	gtgtgttaccaggaagcagtggtgtt----aagtaaaaa...	tgactgaacacatgagga 442
Db	171	AGAAGTGTGTCAACAGACAGATAGTGTATAGAGCAGATATA...	GTATCCACACATATAACAGA 112
QY	443	aatggaaggaagtgtagaagattttaacgggtgcagtggt...	taagaccgtcttcgtga 502
Db	111	ACTGGAGAACAGGTGAGAACACGACAACTTGTGTCGGGGG...	TCAGCCCTGATTTTGTGGTG 52
QY	503	t-ggaanaattcaactatattttaatgcatcagccaga...	ataaacta 552
Db	51	TGGGAATCTCCAATGTATATTCAAATATGATGTGAGAGG...	CCCAACATATA 1
RESULT 15			
LOCUS	AQ207718	505 bp DNA	18-SEP-1998
DEFINITION	HS_3026_B1_D02_77 CIT Approved Human sapiens genomic clone Plate=3026 Col	omic Sperm Library D Homo	ow=H, DNA sequence.
ACCESSION	AQ207718		
VERSION	AO207718.1	GI:3620453	
KEYWORDS	GSS.		
SOURCE	human.		
ORGANISM	Homo sapiens		Vertebrata; Euteleostomi;
REFERENCE	Eukaryota; Metazoa; Chordata; Crania		Mammalia; Eutheria; Primates; Catarrh
AUTHORS	1 (bases 1 to 505)		Wartzell,S., Holzman,T.,
	Mahairas,G.G., Wallace,J.C., Smith,K.		Keller,A., Shaker,R., Furlong,J., Ye
	Food,b.		Zhao,S., Adams,M.D. and
TITLE	Sequence-tagged connectors: A sequen-		approach to mapping and
JOURNAL	Proc. Natl. Acad. Sci. U. S. A. 96 (9739-9744 (1999)
MEDLINE	99380589		
COMMENT	Contact: Mahairas GG, Wallace JC, Ho-		
	High Throughput Sequencing Center		
	University of Washington		
	401 Queen Anne Avenue North, Seattle,		98109, USA
	Tel: (206) 616-3618		
	Fax: (206) 616-3887		
	Email: jwallace@u.washington.edu		
	Sequence Tagged Connector		
	Plate: 3026 row: H column: 3		
	Class: BAC ends		
	High quality sequence stop: 505.		
FEATURES			
source	Location/Qualifiers		
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	/db_xref="taxon:9606"		
	/clone="Plate=3026 Col=3 Row=		
	/clone_lib="CIT Approved Hum		
	/sex="male"		
	/note="Organ: sperm; Vector:		
	E-Coli DH10B"		
	110 a 156 c 92 g 146 t		
	1 others		
BASE COUNT			
ORIGIN			
QY	108	agccacatgaggaagaagaatctctctgagggaagac...	aacacatgattgagacc 167
Db	495	AAGCCACAGAGAAAGCGGAGACTGTCTGGAGCACACACAC...	ATGTACTGAGTGGAGAGC 436
Query Match	14.4%	Score 101.2;	25; Length 505;
Best Local Similarity	59.5%	Pred. No. 7.76	
Matches 286; Conservative	0;	Mismatches	Indels 21; Gaps 6;

